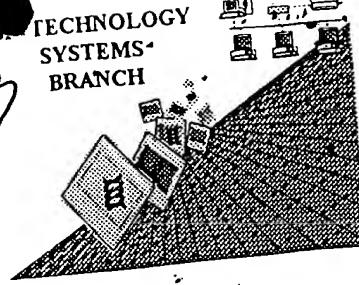


0590  
10/23

0590  
09/88

**RAW SEQUENCE LISTING  
ERROR REPORT**



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/904994

Source: OIPE

Date Processed by STIC: 10/04/01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.  
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:  
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE  
APPLICANT, WITH A NOTICE TO COMPLY or,  
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A  
NOTICE TO COMPLY  
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.  
PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)  
PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

**Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:  
<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

SERIAL NUMBER: 09/904994

ERROR DETECTED

SUGGESTED CORRECTION

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTI

1  Wrapped Nucleic  
       Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2  Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3  Misaligned Amino  
       Numbering

The numbering under each 3<sup>rd</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4  Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5  Variable Length

Sequence(s)  contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6  PatentIn 2.0  
       "bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)  . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7  Skipped Sequences  
       (OLD RULES)

Sequence(s)  missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped

8  Skipped Sequences  
       (NEW RULES)

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences  
Sequence(s)  missing. If intentional, please insert the following lines for each skipped sequence:  
<210> sequence id number  
<400> sequence id number  
000

9  Use of n's or Xaa's  
       (NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represent

10  Invalid <213>  
       Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or Artificial Sequence

11  Use of <220>

Sequence(s)  missing the <220> "Feature" and associated numeric identifiers and responses  
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12  PatentIn 2.0  
       "bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13  Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

OIPE

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/904,994

DATE: 10/04/2001  
TIME: 17:34:16

Input Set : A:\20005661.app  
Output Set: N:\CRF3\10042001\I904994.raw

3 <110> APPLICANT: KUSTERS, Johannes G.  
 4 CATTOLI, Giovanni  
 6 <120> TITLE OF INVENTION: HELICOBACTER FELIS VACCINES  
 8 <130> FILE REFERENCE: KUSTERS  
 10 <140> CURRENT APPLICATION NUMBER: 09/904,994  
 C--> 11 <141> CURRENT FILING DATE: 2001-09-24  
 13 <150> PRIOR APPLICATION NUMBER: EP00202565.8  
 14 <151> PRIOR FILING DATE: 2000-07-17  
 16 <160> NUMBER OF SEQ ID NOS: 21  
 18 <170> SOFTWARE: PatentIn Ver. 2.1  
 20 <210> SEQ ID NO: 1  
 21 <211> LENGTH: 2883  
 22 <212> TYPE: DNA  
 23 <213> ORGANISM: Helicobacter felis  
 25 <220> FEATURE:  
 26 <221> NAME/KEY: CDS  
 27 <222> LOCATION: (206)..(886)  
 29 <220> FEATURE:  
 30 <221> NAME/KEY: CDS  
 31 <222> LOCATION: (897)..(2603)  
 33 <400> SEQUENCE: 1  
 34 rggagatttcccarcaactt caagcacata ttgatccgt gttgtgggtg gtaaattrcr 60  
 36 acttgttaat rctattatta attttttaat aattacttat tatcatatat aataatatta 120  
 38 ttacttataat taaaaaggta ataaaaaggta acgaaattag gactataatc ccattgcctt 180  
 40 taaaatttaa cacaaggagt aatag gtg aaa ctc aca ccc aaa gag caa gaa 232  
 Val Lys Leu Thr Pro Lys Glu Gln Glu  
 41 1 5  
 42 280  
 44 aag ttc ttg tta tat tat gcg ggc gaa gtg gct aga aag cgc aaa gca 280  
 45 Lys Phe Leu Leu Tyr Tyr Ala Gly Glu Val Ala Arg Lys Arg Lys Ala 25  
 46 10 15 20 328  
 48 gag ggc tta aag ctc aac caa ccc gaa gcc att gct tac att agt gcc 328  
 49 Glu Gly Leu Lys Leu Asn Gln Pro Glu Ala Ile Ala Tyr Ile Ser Ala  
 50 30 35 40 376  
 52 cat att atg gac gaa gcg cgc cgt gga aaa aaa acc gtt gcc cag ctt 376  
 53 His Ile Met Asp Glu Ala Arg Arg Gly Lys Lys Thr Val Ala Gln Leu 55  
 54 45 50 424  
 56 atg gaa gag tgc atg cac ttt ttg aaa aaa gat gaa gta atg ccc ggg 424  
 57 Met Glu Glu Cys Met His Phe Leu Lys Lys Asp Glu Val Met Pro Gly  
 58 60 65 70 472  
 60 gtt ggt aat atg gtt ccc gat cta ggt gta gaa gcc acc ttt cct gat 472  
 61 Val Gly Asn Met Val Pro Asp Leu Gly Val Glu Ala Thr Phe Pro Asp  
 62 75 80 85 520  
 64 ggt acg aaa ctt gta act gtg aat tgg ccc atc gaa cca gat gag cac 520  
 65 Gly Thr Lys Leu Val Thr Val Asn Trp Pro Ile Glu Pro Asp Glu His 105  
 66 90 95 100 568  
 68 ttc aaa gcg ggc gaa gtt aaa ttt ggt tgc gat aaa gac atc gag ctc 568  
 69 Phe Lys Ala Gly Glu Val Lys Phe Gly Cys Asp Lys Asp Ile Glu Leu

*Does Not Comply  
Corrected Diskette Needed*

*See Page 6 of 8 A  
As well as Error  
Summary Sheet*

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/904,994

DATE: 10/04/2001  
TIME: 17:34:16

Input Set : A:\20005661.app  
Output Set: N:\CRF3\10042001\I904994.raw

70	110	115	120	
72	aat gca ggc aaa gaa gta acc gaa ctt gag gtt act aat gaa ggg cct			616
73	Asn Ala Gly Lys Glu Val Thr Glu Leu Glu Val Thr Asn Glu Gly Pro			
74	125	130	135	
76	aaa tcc ttg cat gtg ggt agc cat ttc cac ttc ttt gaa gct aac aag			664
77	Lys Ser Leu His Val Gly Ser His Phe His Phe Glu Ala Asn Lys			
78	140	145	150	
80	gca cta aaa ttc gat cgt gaa aaa gcc tat ggc aaa cgc cta gat att			712
81	Ala Leu Lys Phe Asp Arg Glu Lys Ala Tyr Gly Lys Arg Leu Asp Ile			
82	155	160	165	
84	ccc tct ggc aac acg cta cgc att ggg gca gga caa acc cgc aaa gtg			760
85	Pro Ser Gly Asn Thr Leu Arg Ile Gly Ala Gly Gln Thr Arg Lys Val			
86	170	175	180	185
88	cag ttg att cct ctt ggt ggc agt aaa aaa gtg att ggc atg aac ggg			808
89	Gln Leu Ile Pro Leu Gly Gly Ser Lys Lys Val Ile Gly Met Asn Gly			
90	190	195	200	
92	ctt gtg aat aac atc gcg gat gaa cgc cat aaa cat aaa gcg ctt gac			856
93	Leu Val Asn Asn Ile Ala Asp Glu Arg His Lys His Lys Ala Leu Asp			
94	205	210	215	
96	aag gcg aaa tct cac gga ttt atc aag taa ggagactccc atg aaa atg			905
97	Lys Ala Lys Ser His Gly Phe Ile Lys		Met Lys Met	
W--> 98	220	225	230	04
100	aaa aaa caa gaa tat gta aat acc tac gga ccc acc aaa ggc gat aaa			953
101	Lys Lys Gln Glu Tyr Val Asn Thr Tyr Gly Pro Thr Lys Gly Asp Lys			
W--> 102	235	240	245	
104	gtg cgc tta gga gat acc gat ctt tgg gca gaa gta gaa cat gac tat			1001
105	Val Arg Leu Gly Asp Thr Asp Leu Trp Ala Glu Val Glu His Asp Tyr			
W--> 106	250	255	260	
108	acc acc tat ggc gaa gaa ctt aaa ttt ggc gcg ggt aaa act atc cgt			1049
109	Thr Thr Tyr Gly Glu Glu Leu Lys Phe Gly Ala Gly Lys Thr Ile Arg			
W--> 110	265	270	275	
112	gag ggt atg ggt cag agc aat agc cct gat gaa aac acc cta gat tta			1097
113	Glu Gly Met Gly Gln Ser Asn Ser Pro Asp Glu Asn Thr Leu Asp Leu			
W--> 114	280	285	290	
116	gtc atc act aac gcg atg att atc gac tac acc ggg att tac aaa gcc			1145
117	Val Ile Thr Asn Ala Met Ile Ile Asp Tyr Thr Gly Ile Tyr Lys Ala			
W--> 118	295	300	305	310
120	gac att ggg att aaa aac ggc aaa atc cat ggc att ggc aag gca gga			1193
121	Asp Ile Gly Ile Lys Asn Gly Lys Ile His Gly Ile Gly Lys Ala Gly			
W--> 122	315	320	325	
124	aac aag gac atg caa gat ggc gta agc cct cat atg gtc gtg ggt gtg			1241
125	Asn Lys Asp Met Gln Asp Gly Val Ser Pro His Met Val Val Gly Val			
W--> 126	330	335	340	
128	ggc aca gaa gca cta gca ggg gaa ggt atg att att acc gct ggg gga			1289
129	Gly Thr Glu Ala Leu Ala Gly Glu Gly Met Ile Ile Thr Ala Gly Gly			
W--> 130	345	350	355	
132	atc gat tca cac acc cac ttc ctt tct cca caa ttc cct acc gct			1337
133	Ile Asp Ser His Thr His Phe Leu Ser Pro Gln Gln Phe Pro Thr Ala			
W--> 134	360	365	370	

RAW SEQUENCE LISTING  
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136	cta	gcc	aat	ggc	gtt	aca	acc	atg	ttt	gga	ggc	ggc	aca	ggt	cct	gta		1385
137	Leu	Ala	Asn	Gly	Val	Thr	Thr	Met	Phe	Gly	Gly	Gly	Thr	Gly	Pro	Val		
W--> 138	375					380				385						390		
140	gat	ggc	acg	aat	gcg	act	act	atc	act	ccg	ggc	aaa	tgg	aac	ttg	cac		1433
141	Asp	Gly	Thr	Asn	Ala	Thr	Thr	Ile	Thr	Pro	Gly	Lys	Trp	Asn	Leu	His		
W--> 142						395				400						405		
144	cgc	atg	ttg	cgc	gca	gca	gaa	gag	tat	tct	atg	aat	gtg	ggc	ttt	ttg		1481
145	Arg	Met	Leu	Arg	Ala	Ala	Glu	Glu	Tyr	Ser	Met	Asn	Val	Gly	Phe	Leu		
W--> 146						410				415						420		
148	ggc	aaa	ggc	aat	agc	tct	agc	aaa	aaa	caa	ctt	gta	gaa	caa	gta	gaa		1529
149	Gly	Lys	Gly	Asn	Ser	Ser	Ser	Ser	Lys	Lys	Gln	Leu	Val	Glu	Gln	Val	Glu	
W--> 150						425				430						435		
152	gcg	ggc	gcf	att	ggt	ttt	aaa	ttg	cat	gaa	gac	tgg	ggc	aca	aca	cca		1577
153	Ala	Gly	Ala	Ile	Gly	Phe	Lys	Leu	His	Glu	Asp	Trp	Gly	Thr	Thr	Pro		
W--> 154						440				445						450		
156	agt	gcf	atc	gat	cac	tgc	ttg	agc	gtg	gca	gat	gaa	tac	gat	gtg	caa		1625
157	Ser	Ala	Ile	Asp	His	Cys	Leu	Ser	Val	Ala	Asp	Glu	Tyr	Asp	Val	Gln		
W--> 158						455				460						470		
160	gtt	tgt	atc	cac	acc	gat	aca	gtc	aat	gag	gca	ggt	tat	gta	gat	gac		1673
161	Val	Cys	Ile	His	Thr	Asp	Thr	Val	Asn	Glu	Ala	Gly	Tyr	Val	Asp	Asp		
W--> 162						475				480						485		
164	acc	cta	aat	gca	atg	aac	ggg	cgc	gcc	atc	cat	gcc	tac	cac	att	gag		1721
165	Thr	Leu	Asn	Ala	Met	Asn	Gly	Arg	Ala	Ile	His	Ala	Tyr	His	Ile	Glu		
W--> 166						490				495						500		
168	gga	gcf	ggt	gga	gga	cac	tca	cct	gat	gtt	atc	acc	atg	gca	ggc	gag		1769
169	Gly	Ala	Gly	Gly	Gly	His	Ser	Pro	Asp	Val	Ile	Thr	Met	Ala	Gly	Glu		
W--> 170						505				510						515		
172	ctc	aat	att	cta	ccc	tcc	tcc	acc	acc	ccc	act	att	ccc	tat	acc	att		1817
173	Leu	Asn	Ile	Leu	Pro	Ser	Ser	Thr	Thr	Pro	Thr	Ile	Pro	Tyr	Thr	Ile		
W--> 174						520				525						530		
176	aat	acg	gtt	gca	gaa	cac	tta	gac	atg	ctc	atg	aca	tgc	cac	cta		1865	
177	Asn	Thr	Val	Ala	Glu	His	Leu	Asp	Met	Leu	Met	Thr	Cys	His	His	Leu		
W--> 178						535				540						550		
180	gac	aaa	cgc	atc	cgc	gag	gat	tta	caa	ttt	tct	caa	agc	cgt	atc	cgc		1913
181	Asp	Lys	Arg	Ile	Arg	Glu	Asp	Leu	Gln	Phe	Ser	Gln	Ser	Arg	Ile	Arg		
W--> 182						555				560						565		
184	ccc	ggc	tct	atc	cgc	gct	gaa	gat	gtg	ctc	cat	gat	atg	ggt	gtg	atc		1961
185	Pro	Gly	Ser	Ile	Ala	Ala	Glu	Asp	Val	Leu	His	Asp	Met	Gly	Val	Ile		
W--> 186						570				575						580		
188	gcf	atg	aca	agc	tcg	gat	tcg	caa	gca	atg	ggg	cgt	gca	ggc	gaa	gtg		2009
189	Ala	Met	Thr	Ser	Asp	Ser	Gln	Ala	Met	Gly	Arg	Ala	Gly	Glu	Val			
W--> 190						585				590						595		
192	att	cct	cga	act	tgg	cag	act	gcf	gat	aag	aat	aaa	aaa	gaa	ttt	ggt		2057
193	Ile	Pro	Arg	Thr	Trp	Gln	Thr	Ala	Asp	Lys	Asn	Lys	Lys	Glu	Phe	Gly		
W--> 194						600				605						610		
196	aag	ctt	cct	gaa	gat	ggc	aaa	gat	aac	gat	aat	ttc	cgc	att	aag	cgc		2105
197	Lys	Leu	Pro	Glu	Asp	Gly	Lys	Asp	Asn	Asp	Asn	Phe	Arg	Ile	Lys	Arg		
W--> 198						615				620						625		630
200	tac	atc	tcc	aaa	tac	act	atc	aac	ccc	gct	ttg	acc	cac	ggc	gtg	agc		2153

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/904,994

DATE: 10/04/2001  
TIME: 17:34:16

Input Set : A:\20005661.app  
Output Set: N:\CRF3\10042001\I904994.raw

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204	gag	tat	atc	ggc	tct	gtg	gaa	gag	ggc	aag	atc	gcc	gac	ttg	gtg	gtg	
205	Glu	Tyr	Ile	Gly	Ser	Val	Glu	Glu	Gly	Lys	Ile	Ala	Asp	Leu	Val	Val	
W--> 206				650				655				660					2249
208	tgg	aat	cct	gcc	ttt	ttt	ggc	gta	aaa	ccc	aaa	atc	gtg	atc	aaa	ggc	
209	Trp	Asn	Pro	Ala	Phe	Phe	Gly	Val	Lys	Pro	Lys	Ile	Val	Ile	Lys	Gly	
W--> 210				665				670			675						2297
212	ggt	atg	gtg	gtc	ttc	tct	gaa	atg	ggc	gat	tct	aac	gcg	tct	gtg	ccc	
213	Gly	Met	Val	Val	Phe	Ser	Glu	Met	Gly	Asp	Ser	Asn	Ala	Ser	Val	Pro	
W--> 214				680				685			690						2345
216	act	ccc	caa	ccg	gtt	tat	tac	cgc	gaa	atg	ttt	ggg	cat	cac	ggc	aag	
217	Thr	Pro	Gln	Pro	Val	Tyr	Tyr	Arg	Glu	Met	Phe	Gly	His	His	Gly	Lys	
W--> 218				695				700			705			710			2393
220	gcg	aaa	ttt	gac	acc	agc	atc	act	ttt	gtt	tcc	aaa	gtc	gcc	tat	gaa	
221	Ala	Lys	Phe	Asp	Thr	Ser	Ile	Thr	Phe	Val	Ser	Lys	Val	Ala	Tyr	Glu	
W--> 222				715				720			725						2441
224	aat	ggc	gtg	aaa	gaa	aag	ctg	ggc	tta	gag	cgc	caa	gtt	cta	ccg	gtc	
225	Asn	Gly	Val	Lys	Glu	Lys	Leu	Gly	Leu	Glu	Arg	Gln	Val	Leu	Pro	Val	
W--> 226				730				735			740						2489
228	aaa	aac	tgc	cgt	aac	atc	acc	aag	aaa	gac	ttc	aag	ttc	aac	gac	aaa	
229	Lys	Asn	Cys	Arg	Asn	Ile	Thr	Lys	Lys	Asp	Phe	Lys	Phe	Asn	Asp	Lys	
W--> 230				745				750			755						2537
232	acg	gca	aaa	atc	acc	gtc	gat	ccg	aaa	acc	ttc	gag	gtc	ttt	gta	gat	
233	Thr	Ala	Lys	Ile	Thr	Val	Asp	Pro	Lys	Thr	Phe	Glu	Val	Phe	Val	Asp	
W--> 234				760				765			770						2585
236	ggc	aaa	ctc	tgc	acc	tct	aaa	ccc	acc	tcg	caa	gtg	cct	cta	gcc	cag	
237	Gly	Lys	Leu	Cys	Thr	Ser	Lys	Pro	Thr	Ser	Gln	Val	Pro	Leu	Ala	Gln	
W--> 238				775				780			785			790			2633
240	cgc	tac	act	ttc	ttc	tag	gcacaatgcc	ccctttgggg	gcaggttatt								
241	Arg	Tyr	Thr	Phe	Phe												
W--> 242				795													
244	ttaggaatct	tcatcaaacg	cacctgcaat	cggtcttgcg	tgtgcgatcg	tgtcgcttta											2693
246	aaacacaactt	tcatctttaa	gcaatcgcca	tttttaatta	atttaatct	tataattaat											2753
248	attatattat	gccccctcat	ttttaaagga	gaattatgcg	taggtcttgc	gtattgctat											2813
250	gtgggggttg	tttggtgctg	ggcgcaaagg	gtattgaaac	ccatcgccctc	aaaaaaagttag											2873
252	aagccacagg																2883
255	<210>	SEQ ID NO:	2														
256	<211>	LENGTH:	226														
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258	<213>	ORGANISM:	Helicobacter felis														
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263	Gly	Glu	Val	Ala	Arg	Lys	Arg	Lys	Ala	Glu	Gly	Leu	Lys	Leu	Asn	Gln	
264					20					25			30				
265	Pro	Glu	Ala	Ile	Ala	Tyr	Ile	Ser	Ala	His	Ile	Met	Asp	Glu	Ala	Arg	
266					35					40			45				
267	Arg	Gly	Lys	Lys	Thr	Val	Ala	Gln	Leu	Met	Glu	Glu	Cys	Met	His	Phe	

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/904,994

DATE: 10/04/2001  
TIME: 17:34:16

Input Set : A:\20005661.app  
Output Set: N:\CRF3\10042001\I904994.raw

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268      50          55          60
269 Leu Lys Lys Asp Glu Val Met Pro Gly Val Gly Asn Met Val Pro Asp
270   65           70           75           80
271 Leu Gly Val Glu Ala Thr Phe Pro Asp Gly Thr Lys Leu Val Thr Val
272           85           90           95
273 Asn Trp Pro Ile Glu Pro Asp Glu His Phe Lys Ala Gly Glu Val Lys
274           100          105          110
275 Phe Gly Cys Asp Lys Asp Ile Glu Leu Asn Ala Gly Lys Glu Val Thr
276           115          120          125
277 Glu Leu Glu Val Thr Asn Glu Gly Pro Lys Ser Leu His Val Gly Ser
278           130          135          140
279 His Phe His Phe Glu Ala Asn Lys Ala Leu Lys Phe Asp Arg Glu
280 145           150           155           160
281 Lys Ala Tyr Gly Lys Arg Leu Asp Ile Pro Ser Gly Asn Thr Leu Arg
282           165          170          175
283 Ile Gly Ala Gly Gln Thr Arg Lys Val Gln Leu Ile Pro Leu Gly Gly
284           180          185          190
285 Ser Lys Lys Val Ile Gly Met Asn Gly Leu Val Asn Asn Ile Ala Asp
286           195          200          205
287 Glu Arg His Lys His Lys Ala Leu Asp Lys Ala Lys Ser His Gly Phe
288           210          215          220
289 Ile Lys
290 225
293 <210> SEQ ID NO: 3
294 <211> LENGTH: 568
295 <212> TYPE: PRT
296 <213> ORGANISM: Helicobacter felis
298 <400> SEQUENCE: 3
299 Met Lys Met Lys Lys Gln Glu Tyr Val Asn Thr Tyr Gly Pro Thr Lys
300 1           5           10           15
301 Gly Asp Lys Val Arg Leu Gly Asp Thr Asp Leu Trp Ala Glu Val Glu
302 20          25          30
303 His Asp Tyr Thr Thr Tyr Gly Glu Glu Leu Lys Phe Gly Ala Gly Lys
304 35          40          45
305 Thr Ile Arg Glu Gly Met Gly Gln Ser Asn Ser Pro Asp Glu Asn Thr
306 50          55          60
307 Leu Asp Leu Val Ile Thr Asn Ala Met Ile Ile Asp Tyr Thr Gly Ile
308 65          70          75          80
309 Tyr Lys Ala Asp Ile Gly Ile Lys Asn Gly Lys Ile His Gly Ile Gly
310 85          90          95
311 Lys Ala Gly Asn Lys Asp Met Gln Asp Gly Val Ser Pro His Met Val
312 100         105         110
313 Val Gly Val Gly Thr Glu Ala Leu Ala Gly Glu Gly Met Ile Ile Thr
314 115         120         125
315 Ala Gly Gly Ile Asp Ser His Thr His Phe Leu Ser Pro Gln Gln Phe
316 130         135         140
317 Pro Thr Ala Leu Ala Asn Gly Val Thr Thr Met Phe Gly Gly Gly Thr
318 145         150         155         160
319 Gly Pro Val Asp Gly Thr Asn Ala Thr Thr Ile Thr Pro Gly Lys Trp

```

<210> 10  
<211> 2407  
<212> DNA  
<213> Helicobacter felis

<220>  
<221> CDS  
<222> (2)..(682)

<220>  
<221> CDS  
<222> (693)..(2399)

<400> 10

ccc gcc tct gaa gtg cct cta gcc cag cgc tac act ttc ttc tag 2399  
Pro Ala Ser Glu Val Pro Leu Ala Gln Arg Tyr Thr Phe Phe  
785 790 795

(gcncaatg) 2407

<210> 11  
<211> 226  
<212> PRT  
<213> Helicobacter felis

Errored: As you can see sequence 10 includes sequence 10 includes unknown nucleotides. It is required that you describe unknowns in fields 221, 222 and 223.

The type of errors shown <sup>may</sup> exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/904,994

DATE: 10/04/2001  
TIME: 17:34:17

Input Set : A:\20005661.app  
Output Set: N:\CRF3\10042001\I904994.raw

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:98 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:102 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:106 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:110 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:114 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:118 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:122 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:126 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:130 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:134 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:138 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:142 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:146 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:150 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:154 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:158 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:162 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:166 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:170 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:174 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:178 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:182 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:186 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:190 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:194 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:198 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:202 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:206 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:210 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:214 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:218 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:222 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:226 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:230 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:234 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:238 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:242 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4  
L:446 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4  
L:450 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4  
L:454 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4  
L:458 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4  
L:462 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4  
L:466 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4  
L:470 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4  
L:474 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4  
L:478 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4  
L:482 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/904,994

DATE: 10/04/2001  
TIME: 17:34:17

Input Set : A:\20005661.app  
Output Set: N:\CRF3\10042001\I904994.raw

L:486 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4  
L:490 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4  
L:494 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4  
L:1232 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:10  
L:1232 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10